AMENDMENTS TO THE SPECIFICATION

Please insert the following paragraph beginning at page 1, line 4 of the Specification and before the "Field of theInvention" section:

INCORPORATION-BY-REFERENCE OF SEQUENCE LISTING

The contents of the text file named "41228_TM10001US_SeqList.txt," which was created on December 15, 2010 and is 15 KB in size, are hereby incorporated by reference in their entirety.

Please amend the following paragraph beginning at page 18, line 16 of the Specification, as follows:

An example of such an alignment for a random set of selected 7TM receptor human sequences is shown in the table below. For this illustration, the sequences and identification codes for the 7TM receptors are retrieved from ~~www.gper.org~~ Molecular Class-Specific Information System (MCSIS) project. The amino acid residues, in sequential or non-sequential order, are selected from different helices located in the binding site. For GPR44, the following amino acid residues, up to six per helix, from TM-III, TM-IV, TM-V, TM-VI and TM-VIII. have been selected. In an specific example given below, the selected residues for TM-VII correspond to VII-02 (Leu), VII-06 (Thr) and VII-09 (Ala) in the generic numbering. The rest are assigned analogously as described above.

	TM Helix:	III	IV	V	VI	VII
SEQ ID No. 1	GP44_HUMAN	HSFFMF	NTY	AKFA	WYHSEA	LTA

Please amend the following paragraph beginning at page 18, line 28 of the Specification, as follows:

The amino acid residues, e.g. up to six per helix, in sequential or non-sequential order, are selected from III-04 to VII-09 to form the following 22 amino acid pseudo-sequences, which are used in the alignment and subsequent comparison.

GP44_HUMAN (SEQ ID No. 1) HSFFMFNTYAKFAWYHSEALTA

O2T1_HUMAN (SEQ ID No. 2) QHYLVGDGLSINFLFSLYAKVT

O7C2_HUMAN (SEQ ID No. 3) QIFIGCGSETEIFVLCLYSLVT

B3AR_HUMAN (SEQ ID No. 4) WTDVVTVSPVSSSWFFNRAFNG

PE24_HUMAN (SEQ ID No. 5) STLLSLTTTAASSSLVVNQDIA

APJ_HUMAN (SEQ ID No. 6) SSIFMYLAVGSTGWYHKYMFTS

O1E1_HUMAN (SEQ ID No. 7) QMFLGDHAHACFDVFLLYATMT

FML2_HUMAN (SEQ ID No. 8) VHIDLFLTNLHFGWYEGMAISA

ACTR_HUMAN (SEQ ID No. 9) IDFVLLTGMVVITWFVVMTFGI

5H4_HUMAN (SEQ ID No. 10) RTDVTTISPACSAWFFNDPWLG

NFF2_HUMAN (SEQ ID No. 11) SGQGVAIMSTVYRWLWMSDYHA

O2B2_HUMAN (SEQ ID No. 12) QLFLGSNSQHVDFLVTLYAKLG

AG2R_HUMAN (SEQ ID No. 13) ASVSLYASAGKNGWHQTDVMIA

O5U1_HUMAN (SEQ ID No. 14) QVFIASSGHKIHFRSARVFLVT

1019_HUM (SEQ ID No. 15) NLLSRTLNLHLYEFSIGSMFLT

C3X1_HUMAN (SEQ ID No. 16) TTFFFFVAQNTNGWYNIETLEA

5H6_HUMAN (SEQ ID No. 17) WTDVCSASPVASTWFFNQAFTG

BRB2_HUMAN (SEQ ID No. 18) VNISLYLSMNLNGWFQTDTTSA

O2F2_HUMAN (SEQ ID No. 19) QLSLGGNSQPTNIMFCLYIKVA

NMBR_HUMAN (SEQ ID No. 20) IPQLVGLAESIFYWNHYRSTRS

OXI2_HUMAN (SEQ ID No. 21) QMIHSMARISLSYYMISHRVNL

NTR2_HUMAN (SEQ ID No. 22) YYHEAYLAMINVSWYHRYCYNF

AG2S_HUMAN (SEQ ID No. 23) ASVSLYASAGKNGWHQTDVMIA

5H2A_HUMAN (SEQ ID No. 24) WIDVSTISIVGSSWFFNAVLVG

GP72_HUMAN (SEQ ID No. 25) SRQYLHFSHDTFLWLNVLSYHA

ACM1_HUMAN (SEQ ID No. 26) WLDYSNLWATTAAWYNVSTWYC

CKRA_HUMAN (SEQ ID No. 27) ISYSFHLAAAQVGQYSLDTLSA

TA2R_HUMAN (SEQ ID No. 28) MGMIGLLGPSLSLWLLITVLLA

OYD1_HUMAN (SEQ ID No. 29) QMVHYARRYGVAAYAFFHRINV

LGR5_HUMAN (SEQ ID No. 30) IGSISEKYSLLNCNVASSLKLV

O5V1_HUMAN (SEQ ID No. 31) QLFVVGNSHNINFWFLVYIRVS

FSHR_HUMAN (SEQ ID No. 32) AGTVSEAAPVCLDMISAASKVH
DADR_HUMAN (SEQ ID No. 33) WVDISTISPASSSWFFNLPFVG
GRPR_HUMAN (SEQ ID No. 34) IPQLVGLAESSFFWNHYRSSRA
AG22_HUMAN (SEQ ID No. 35) FGLTMFSSTAKNGWFHTDALIG
O2D2_HUMAN (SEQ ID No. 36) RLFLGCVSDSIAFLVFLYGKVA
O4F3_HUMAN (SEQ ID No. 37) QIIHGGHSQPLDYFPMYPHKIA
O2H3_HUMAN (SEQ ID No. 38) QIFLGTAWGQSTLVLSLYGKLA
HH1R_HUMAN (SEQ ID No. 39) WLDYSTWVIKTANWYFFIAHIG
CML1_HUMAN (SEQ ID No. 40) SNLIMFLSSTRFGWYHNELLTA
EBI2_HUMAN (SEQ ID No. 41) TAFYTYQTLLACGFYHIHMLVM
O2G1_HUMAN (SEQ ID No. 42) QMALGGSAYAIRLHSNRALNVT
ETBR_HUMAN (SEQ ID No. 43) VPQKVGLAEDLFYWLHRKLDIA
GPR1_HUMAN (SEQ ID No. 44) VFTVLDIGATKFGWYHSELITA
FML1_HUMAN (SEQ ID No. 45) IHVDLFLTVGRFGWFQAGTVSA
NK4R_HUMAN (SEQ ID No. 46) QNPIVFLAQHVIVWYHFTAYFA
GPR81_HUMA (SEQ ID No. 47) GLLARAGTLHMFEYSVRFLLLT
GPR6_HUMAN (SEQ ID No. 48) TVLVFALGPLRASWFACGSTLA

Please amend the following paragraph beginning at page 29, line 31 of the Specification, as follows:

In one embodiment, the amino acid residues, up to six per helix, are selected from TM-III, TM-IV, TM-V, TM-VI and TM-VIII to form the following pseudo-sequences, which are used in the alignment. The following rank order of the similarity of the receptors can be obtained by implying the given set of amino acids associated with theoretically derived physicochemical descriptors reflecting hydrophobic, electronic, steric, and hydrogen bonding properties:

	Receptor:	Pseudosequence	Ranking
(SEQ ID No. 1)	GP44_HUMAN	HSFFMFNTYAKFAWYHSEALTA	1
(SEQ ID No. 35)	AG22_HUMAN	FGLTMFSSTAKNGWFHTDALIG	2
(SEQ ID No. 40)	CML1_HUMAN	SNLIMFLSSTRFGWYHNELLTA	3
(SEQ ID No. 18)	BRB2_HUMAN	VNISLYLSMNLNGWFQTDTTSA	4

(SEQ ID No. 27)	CKRA_HUMAN	ISYSFHLAAAQVGQYSLDTLSA	5
(SEQ ID No. 16)	C3X1_HUMAN	TTFFFFVAQNTNGWYNIETLEA	6
(SEQ ID No. 13)	AG2R_HUMAN	ASVSLYASAGKNGWHQTDVMIA	7